



RECEIVED

08/852495

AUG 13 1998 SEQUENCE LISTING

(1) GENERAL INFORMATION: ~~RECEIVED
SERVICE CENTER~~

(i) APPLICANT: Ruddy, David A.
Wolff, Roger K.

(ii) TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
HEMOCHROMATOSIS GENE

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pennie & Edmonds, LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036-2811

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/852,495
(B) FILING DATE: 07-MAY-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Poissant, Brian M
(B) REGISTRATION NUMBER: 28,462
(C) REFERENCE/DOCKET NUMBER: 8907-0057-999

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-493-4935
(B) TELEFAX: 650-493-5556
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACACACACA CACACACACA CACACACACA CACACAAATG AGGTATATAA AGGGTCTCCT	60
AAAATGTCAT CTGATATTTG TTATTCATA TTCTCAGATT TTTAATCCAT TTAGGTAGGT	120
CTATTTAGA TAGCCTTGTC TGAAACAGAG CTGGGACCTG ATGAGTGAAA ATGAGCTCAC	180

CAGAAGAAAA	ATCAAACAGG	CATTCAGAG	ATTGAGGCCA	AGAAGTTAAA	TGTCTTAAAT	240
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ACAGCAGAACG	AGGTGAACAG	AGGCCAGAGA	TGGTCACTGA	GTGGGCCCTT	AAGTCATGGT	360
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TACTTTGGAT	TTGTAGAGAT	GAAGGAAATG	TAGCAAGTGA	CACTCTAGA	ATGTTGATT	480
GAGTAAATGG	TAGTGTCACT	TATTGAACGT	GGGAGAACTG	GAAGGGATAA	CAGGCTTAAG	540
GAGCACGTT	ATTCCTGTGT	CTTGGAAAGTG	TTTAGGGTGA	AAGACCTATT	AGAGTTCTAA	600
ATGGAGATGT	CAAGTGAAA	TGTGGCTACA	CACATTTGCA	TTTCAGAAAA	AAGGTCAGGC	660
TGGAGATGTA	AAATTGGAAG	TTTACTGCAT	ATAGATAGTC	TTTGGAAACCG	TAGTATTGAT	720
GAAGCCATTA	ATGAGACAGA	ACAAAGACTA	GGGACCAGAG	CCAAGCTCCA	AGTTTCTAAA	780
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AATGGATATG	GTTATCTGCC	TGGTGTCTGT	GAAATAATT	AAGCCAGGAA	GAGATCCTCA	960
CCAGAAAATG	ACTATGCTGG	CAACTTGGAT	CTTAGATTTC	CAGCCTGCAG	AATTGTTAGA	1020
AAATAAAATGT	CTATCGTTA	AGCCACCACT	CTGTAGTATT	TTGTTATGGC	AGTCCAAGCT	1080
GACTAAGTT	TGGTACCCAG	GCGTGGGATG	CTGCAACAAAC	AAATACCTAA	ACATGGGGAA	1140
GTGGCTTTGG	AAATTGGTGA	TGGGTAAAGG	CTGGAAGAGT	TTGAGGTTCA	TACTAGAAAA	1200
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CGATCATGGA	TAGAATATTA	AATATGCTGG	TTAAAATATG	GACTTAGGC	CAGGCGTGGT	1380
GGCTCACGCC	TGTAATCTCA	GCACTTGGG	AGGCTGAGGG	CACAGATCAC	GAGGTCGGGA	1440
GTTTGAGACC	AGCCTGGCCA	ATATGGGAA	ACCCGTCTC	TACTAAAAT	ACAAAAATT	1500
GCTGGGCATG	GTGATGTGCT	TCTGTGGTCC	CAGCTACTCG	GGAGGCTGAG	GCTGAAGAAT	1560
CGCTTAAACC	CGGGGGGTGG	AGGTTGCAGT	GACCCAAGAT	CACACCACTG	CACTCCAGCC	1620
TGGGATACAG	AGCAGGACTC	CACTCCCCCC	GCCACACACA	CACAAAAAAT	ATATATATAT	1680
GGACATTAAGA	GTCAACTCTT	GTGAGGTCTC	AGATGAAAAT	GAGGGACAGG	TTATTGGAAA	1740
CTGTAGAAAT	CACTGTTCTT	GTTACAATGT	GTCAAGAACT	TGGCTGAATT	ACGCTGTAGT	1800
GTTTACTGGA	AAGAACTTAT	AAGCAGTAAA	ACTGGATATT	TACCAGAAGA	GATGTCTAAG	1860
CAAAGTATTG	AAGGTGTGAT	TTAGGTCTC	CTTACTGCTT	AAAGTGAAAT	GTGAGAGGAA	1920
AGAGCCGAAA	TAAAGAAGGA	ATTTTAAGC	AAAACACAAT	CAGAACTTGG	AGATTGGGA	1980
TAGATTCTC	AATCTATATT	GTAAAAATTG	AGAAAGTTT	TCTTGAAGAG	GTATGGTTGA	2040
ACAATGTTT	CTTTTCTTT	TTTTTCTTG	TTTTTATT	TATTTTATG	TTTTTGAGA	2100
CAGGGTCTGG	CTATGTCATC	CAGGCTGGAG	TGCACTGGCA	CAATCTCAGT	TCAGTGCAAC	2160
CTTGCCTTC	AGGCTCAAGC	AATCCTCCA	CCTCAGCCTC	CTAAGTAGCT	GGGACTACAT	2220

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AAAGTGTGG	GATTACAGGC	GTGAAACACT	GAGCCTAGCC	TGAACAACCA	TTTGATAAAAG			2400
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GCTGTCAATG	TGTACTATT	TTTAAGAAAA	GGAAAGACTG	ACCCACCAAA	GGCAACTTAC			2640
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GTAGGGCAAT	GGTGTGATCT	CAGCTCACTG	CAATCTCCAC	CTCCCAGGTT	CAAGGGATT			2760
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AGAGTACAGA	TGGGATAGGG	TGGGGTGGG	AA	ACATGTAGT	CAAGGCTGAC	TCTACCTGTT		3060
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CCACCAAAC	GAAAGACCGA	GACTTCAGGC	AGGGCAGATG	GAGTAGGCCA	ACTACAGAGC			3180
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CATTGTACCT	TAGAACATG	TAACATTCT	GGTTTCACAC	GTTCAAAGCT	GGAAAGGAAT			3420
TTTGTCTCTG	GATGAATCAC	ACATTGAGCC	TCACCCGTAA	CCTGATTTAG	ATGATTTTT			3480
AGATGACACT	TTGAAC	TTA	GAATTGATG	TAGAATGAGT	TAAGACTT	CCCCGGCTGT		3540
TGGGATGGAA	TAATTTTTT	TTTTTTTG	AGACGGAGTC	TAGCTCTGTC	GCCCAGGCTG			3600
GAGTGCAGTG	GCACCAC	TT	GGCTCACTGC	AAGCTCTGCC	TCCCAGGTT	ATGCCATT		3660
CATGTCTCAG	CCTCCAGAGT	AGCTGGACT	ACAGGCGCCC	GCCACCACGC	CTGGCTAATT			3720
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TGACCTTCTG	ATCCGCCTGC	CTTGGCTTCC	CAAAGTGCTG	GGATTACACG	TGTGAGGCCAC			3840
CATGCCCGGC	TGGGATGGAA	TAAATTATC	TTGTATGGGA	GAAGGACATA	CATTTGGCA			3900
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GAGCTCTCTC	TCCACGCAGG	CACCAAGGAA	ACACCATA	AACACACAGT	GAGATGGCAG			4140
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CATCCAATGA	AGTTCTGACA	TTTCTCAAC	ATGAGTACAG	TAATTCAATG	CCAGAGAATT	4560
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CAACATGGTG	AAACCTGTC	TCTACTATAA	ATATAAAAAT	TAGCTGGGTG	TGGTGGTGCA	4800
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TTAACTGGCA	CCTTCTGTGT	TTCTCTGAAG	CTCCCTTGC	TTAGGGACTA	GGCTCTTAGC	5940
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CAAACGCCA	GTGAAATTG	GATTTTGG	ATATAGTTTC	TTTTTCTTG	TTACTTTTG	6060
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TGATTCTCTT	GCCTCAGCCT	CCCGAGTAGC	TGGGACTACA	GGCGTGCAC	AGCATGCCA	6180
GCTAATT	GTATTTTTA	GTAGAGATGG	GGTGGTTTT	TTTTGAGAC	GGAGTTTCAC	6240
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CGGCTAACCT	GGTGAAACTC	CGTTCTACT	GGTGGCGGGC	GCTTGTAAATC	CCATCTACTA	8340

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GAGATCGCGC CACTGCATTC CAGCTTGGC AACAGGAGCA AAACCTCGTT TCAAAAAAGC	8460
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CACCACGCCA AACTTATTTC TTTATTTATT ATTTTTATT AGTAGAGAGG TGTTTCACCA	8820
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CGGGGGACTA GTCGGAGGAC CAAACAAGGT TACCAACACG TTAGAGTTT GCCTTCAATT	9240
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TGATAGTACG TAACTGACCT ACTATTACAT ACAAACAGAC CAACCTTAG TAACAGCGCT	9420
CCCCAAAAAC CGAAAAGCAG TAATACGCTT TGCTCAAGGT TGGCATAAAA TTAACTTACC	9480
TTAGTGCCTT TTTCCCTCT ACCTACAAGC AGTGAGGTTA GCTCTCCTT TGAAACGGTA	9540
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GCGAGCCGCG TTGCCGGCCA GCTCCAGGAT CTCGGCGGTC AGGTACTCTA ACACCGCCGC	9840
CAGGTACACC GGCGCGCCTG CCCAACCCG CTCTGCGTAG TTGCCTTAC GGAGCAGGCG	9900
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CTTTTATAGG TAGTCCTGG GGAGTAAATC CGACTTTTG ATTGGTCGGT AGCAAATGCT	10140
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GATGACAACG GTGCAGTTG TCTTCCAATT AACTAAGAGG TACTCTCCAT CCCTCATTAG	10260
CATAAAAGCC CTATAAGTAG CAGAAATCCG CTCTTACTT TCGACACATT TCTGGTGT	10320
TAAGATGCCT GAGCCAGCCA AGTCTGCTCC CGCCCCGAAG AAGGGCTCCA AGAAGGCAGT	10380

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CTGTTTCGT	GGCGCACACC	TTCGTAGTAT	ACTGAAGGGT	GTGTCTCCTG	GGTTTCCAAAC	11280
TGCCCGGTA	ATAGTCTTT	AACCTAATAT	GCGTCAGTTT	TGATAACAAAC	ACTAAGGCAG	11340
TACAGAACTA	AAGATGTAAG	CACTGCGCCA	GATGTTGCTT	CATACATCTT	ATTCTATTCA	11400
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AGACAAGTT	GAAAGTTGCT	TTAGGAGAAG	CCAACTCTTA	ACTGCTGGGT	AAATTGACAA	11580
GCCTTCGAAC	ACTGAAC	AGGCCAGTAA	GGACTAGGCG	CTGGTGGGG	GAGAATGAAG	11640
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ACAAC TGCA G	GCCGCTTG	GGCCTGGAA	ATTCCACATT	CCCTTAAGTA	TTTTACTCAT	11760
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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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TGACCTCTG	ATCCGCCTGC	CTTGGCTTCC	CAAAGTGCTG	GGATTACAGG	TGTGAGCCAC	3840
CATGCCCGC	TGGGATGGAA	TAAATTATC	TTGTATGGGA	GAAGGACATA	CATTTGGCA	3900
GGTCAAGGAC	AGAATGTTAT	GGACTAAACT	GTGTCCCCCA	AAATTCAATT	ATTAAAACCC	3960
TAAACCCAG	TGTGACTGCA	TTTGGACATA	GAGCCTTAG	GGGGTACATA	AAACTAAAGA	4020
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GAGCTCTCTC	TCCACGCAGG	CACCAAGGAA	ACACCATACA	AACACACAGT	GAGATGGCAG	4140
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CATGTTGGCT	CCTTTACTCT	GCCCAAACTA	CAACTCAAAC	AAACAACTGT	AATATAATAA	4500
CATCCAATGA	AGTTCTGACA	TTTCTCAAC	ATGAGTACAG	TAATTCAATG	CCAGAGAATT	4560
CATTTTATTT	TGAAATCTAC	ATGCCATATT	CCAATTCTG	TTGAAGATGC	AATGGTTATA	4620
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GCATTTGAGA	GGCTGAGGTG	GGCATATCAC	CTGAGGTCAG	GAGTTGAGA	CCAGGCTGGC	4740
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TGCCTGTAGT	CCCAGTTACT	AGGGAGGCTG	AGGTAGAATT	GCTTGAACCT	GGGAGCAGGA	4860
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GACATATGAG GTTTTGTTT TTTTTTTTT TTGGAGATGC AGTCTCCCTC TGTTGCCGT 229860
GCTGGAGTGC AATGGCGCAA TCTGGCTCA CTGCAACCTC TGCCCTCTGG GTTCAAGCAA 229920
TTCTCCTGCC TCAGCCTTCC AAGTAGCTGG GATTACAGGC ACCCACTACC ACGCCTGGCT 229980
AATTTTGTA TTTCTGGTAG AGACGGGGTT TCACCATGTT GGCCAGGCTG GTCTCGAACT 230040
CCTGACCTCA AGTGATCCAC AATCCTGGC CTCCCAAAGT GCTATGATTA CAAGCATGAG 230100
CCACCTGCC AGCCAGAATA TATGTCATT TTGAGTCCTT TAACAAAGTC ATAAGAATT 230160
TAGGAATTCA GTTACTTTCT TGAGAAAATC TCTGAAAAGA TGCCAATAAT TTGTAGCCAA 230220
TTATATTGAT TTCTCTTTT CATATTGAGA ATTGTTTTT AAAAAGTTG TATGTGTGAA 230280
GATTTTGCA CTGTAGTTAA AGAAACCACC TGTGTGTTGG TTAAGCCATA AGTACATGTA 230340
TTCAAATAAA TTGAGGTGGG GTTACTCTGA GAATCAAAGG AAAACCTGAA GAAACAGGCA 230400
GCCTCAAAAG GTCTTAGCTG TAGCAACTTG CTCCATTGTT GAAATAAAATA GGCTTGAAC 230460
TGTATTTCC CTCTACTCAA CATTAAAGGT CTCAGAAGAT AATATAATTG GTGAAATT 230520
AGTAAAGTGC TCACTCTTT GCTTAACAA ACCCTAGAGA GCTGGTAGGC AGAGCCTCAA 230580
CAGACCGTTT TAGCTTCAA AGGGAGTTCA GGACACCAGT ATTACAGGACC ACAATACATC 230640
ACACATAATT GAGAAAAGAT AGTTCCACCA AATAAAGTTG AAATGCTGAC AAGAAGGGT 230700
AAGAAATCTT GGAAATAGGT TTATATAAA TTTATTTTT CCTTTTTAT TGTTATGGAA 230760
TAGGACCAGT TCTACTTAAG CCACCCATTG GCCAAATAA AGTGAGAAC 230820
GGGACTCCTC TTTGTAGCTC CAAGTGCCAC TAACAATTCT TAGGACCTGA GCTATAAGCC 230880
AGGTGATTC AGTTAATATG ATCAATTATT TCATTAAAT GGCTCTAATG TGCAGAGGGA 230940
ACGGAGCCCA TCAGCATTCC CTGCAGGGAA CTGCAGTGGC TTTTATCAAC TTGAACAGCT 231000
AGCTTCAAC TGTTTGAAA TCACCTTCAG GGTGGTCATG TAGTTGCTT TTTGAAATCA 231060
GAAGATGATT CTGCCTCTT TAATATGTGA CTCCTCAGAT TCAGAAAGTG CTCGCTAGTC 231120
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TGGGGAACT ATCAGAGAAA TTGGTGCAC GGACATAAGA GGAAGGCACA GTGAAGCAGA 231240
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GGAGCATGAA AATCCAGGCC AATCTGGCAC CATGAGCTCT AATTTTGTT GGAGTTCTG 231360
GAACCGATTC TGATGAATGA CTGTTAGCC ATTTTAGAGT GTGGCATAAC TGGCTGCTGG 231420
CATACAGAGG TTGGATGTAA ACGGGCCTT GCCCTCTCTT ATGAACATAG ACAGGAACTA 231480
AACTGTGTCA CATAGGTTCC AAATGGTGGC CTGAATACTA TTTACAACTA AGGTACAATG 231540
AAATTGAGTA AGTCTTTCC TCTTTGCAG ATACCACAT TATTGATATA TTTCTTCAA 231600
GTAACTATT TGTATTTGGT AATTTTAAT AGAAATGTAA TAATTGCTTC TCAAGTTAG 231660
TCTTTAGTCT TAAGGTTGAT GCTCTCCATG TCCTTCCAAA AAAAGGTATG TTGCTTTAT 231720
TATATCCTCG CCTTCAGATG GGATTATTCC ATTTGTTCT TTGTTAATAT ATACTTGAG 231780

CCACTTTTT TGTGGCTCTG GGTGAGATGC TATAGGTACA ATGACAAGTG ATACGTGTGT 231840
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GTATCACACA CCAGCCGTAT GCCAGGCACC ACTCTAGGTG CTAGGGATAC AGCAGTAAAC 231960
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CGGAGTGCTG AGAGCCTTCT TAGTGTGTAT TCAGTGTGTT AAGAGAGCTT GTGGATGAAT 232260
AATAAATAGG ACAAAATTAA TCCAAACTTA AGCCTTGCTT TAGGTAAAAG GGCTCCTCTT 232320
ACAAGGTAGA AGGTTATTAT TTGACATTAA AATCCAAC TG AAGACTAATA AGACTAATTA 232380
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AAGAGATGAA CAAGCCCTGT ATCTGAAGCC ATCATGCCTA GTTATGGTCC CCGACTGTT 232680
ATGATGCCTG GAAGGGAGGC CCCCTGCACC CTAGAAAGCT GGGTGGGTTG TACTGTCTGC 232740
TTTACTGCTA AAAACCCCTCT TCTTGGATC TGGACTTTAC CTCTATCTGA TTTTTTTTTC 232800
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GCCCCATTGC CTCACAGAAA GAATTCATA GCTTCCAGCA TCCTCTCTCC TTCATTATAC 232920
TTTGATTCA GCATTGCTAT TTTTCTCTT GGGTGGTGC GCTCTCTCTC TCCTTCCCAT 232980
GTCTTGGTGG TTTTCTGCTA ACTCCTGCTT TTTTCTTTT TTTTTTTTG AGACGGAGTC 233040
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CACAAATATAT AATCCCTGAT TCCCAAACAC GGTCTTTCA TATACATTTC CCACTGTACA 233340
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CTTAACAAAT AGTCTGACAC AAAGTGGATA TAACAATATT TTGAATTATG AATAACTAAA 233880
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CATTGGGGCC AAATCTTAGA TCATGTAAAT TTTCTTCTAT ATTTTATTCT AAAAGCTTGT 235920
AATGTTGAT ACATTCTAAA AGATGTAATG TTTGATACAT TACATCTAGT CCTTGATTT 235980
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TGTGTGTGTG TGTGTGTGTG TGTGTG 237326

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTTAGAACG CGGCTACAAT

20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCGATTACAT TAATGCAGGT

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTAAAACG ACGGCCAGTC

20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCAGGAAACA GCTATGACC

19

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCATCAGCGA TTAACCTTCTA C

21

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTGCATTGTG GTGAAATCAG GG

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGAGTAATT GTTTAAGGTG C

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGAGTAATT GTTTAAGGTG T

21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGAAGAGATA GATATGGTGG

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATGTGACC GTCCCATGAG

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAACTGAATA TGCAGAAAAA AGTACACC

28

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGTAGCTGGG ACTCACGGTG T

21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGTAGCTGGG ACTCACGGTG C

21

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGCCACCA C TCCCAGCTCA T

21

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TATATATATA TATA

14

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAAAAAA AAAA

14

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGGATGGTCT

10

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTGTTGTTGT TG

12

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTTTTTTTTT TTTT

14

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AATAATAATA AT

12

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTTTTTTTTT T

11

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATATATATAT ATATATATAT

20